

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2002, 17:31:55 ; Search time 1398.01 Seconds
(without alignments)
8543.543 Million cell updates/sec

Title: US-09-762-633-3
724

Perfect score: 1 gaagtcgtacaaagtgagcc.....gatgtatarggaagttaaca 724

Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	724	100.0	724	1	AB022061
2	318.8	44.0	624	1	AB022063
3	238.4	32.9	399	1	AB022062
4	169	23.3	579	1	AB022094
5	163.8	22.6	442	1	AB022064
6	119.2	16.5	467	1	AB040730
7	117.6	16.2	467	1	AB040727
8	117.4	16.2	417	1	AB040726
9	117.4	16.2	417	1	AB040737
10	114.2	15.8	413	1	AB040729
11	113.8	15.7	505	1	AB040724
12	111.8	15.4	5986	1	CJ16SRNA
13	111.8	15.4	308601	1	CJ11168X2
14	111.8	15.4	314150	1	CJ11168X1
15	111.8	15.4	317511	1	CJ11168X3
16	110.4	15.2	460	1	AB040723
17	110.4	15.2	968	1	AF146727
18	108.8	15.0	441	1	AB040542
19	108.8	15.0	479	1	AB040714
20	108.8	15.0	551	1	AB040717
21	106	14.6	556	1	AB040720
22	102.8	14.2	750	1	AB074835
23	102.8	14.2	751	1	AF074830
24	102.8	14.2	914	1	AF074830
25	102.8	14.2	946	1	AF074839
26	102.6	14.2	2423	1	AB066098
27	102	14.1	751	1	AF074832
28	101.8	14.1	752	1	AF074834
29	101.6	14.0	753	1	AF074828
30	101.4	14.0	751	1	AF074833
31	100.4	13.9	778	1	AF074831
32	100.4	13.9	778	1	AF074836
33	100.4	13.9	823	1	AF074837
34	100	13.8	812	1	AF074838
35	99.6	13.8	632	1	AF074829
36	97	13.4	632	1	AF074841
37	94.4	13.0	511	1	AF203394
38	94	13.0	493	1	AB004288
39	94	13.0	493	1	AF035441
40	94	13.0	494	1	AB004284
41	94	13.0	494	1	AB004289
42	94	13.0	502	1	AF279422
43	94	13.0	502	1	AF279423
44	94	13.0	502	1	AF279424
45	94	13.0	502	1	AF279425

ALIGNMENTS

RESULT 1
LOCUS AB022061 724 bp DNA BCT 30-MAR-2000
DEFINITION Pectinatus cerevisiiphilus DNA, 16S/23S rRNA intergenic spacer
ACCESSION AB022061
VERSION AB022061.1 GI:7288087
SOURCE
ORGANISM Pectinatus cerevisiiphilus (strain DSM20467) DNA.
Pectinatus cerevisiiphilus
Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa
subbranch; Selenomonadaceae; Pectinatus.
REFERENCE
1 (sites)
Motoyama, Y. and Ogata, T.
16S-23S rDNA spacer of Pectinatus, Selenomonas and Zymophilus
reveal new phylogenetic relationships between these genera
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 883-886 (2000)
JOURNAL MEDLINE
20222199
2 (bases 1 to 724)
Ogata, T. and Motoyama, Y.

TITLE Direct Submission
Submitted (07-JAN-1999) to the DDBJ/EMBL/GenBank databases

Ogata, Asahi Breweries, Ltd., Brewing Research and Development Laboratory, 1-1-21, Midori, Moriga, Ibaraki 302-0106, Japan
(E-mail: tomo.ogata@asahibeer.co.jp, Tel: 81-297-46-1513,
Fax: 81-297-46-1514)

FEATURES	Location/Qualifiers
source	1. .724

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/misc_feature
1. .724
/organism="Pectinatus cerevisiiphilus"
/strain="DSM20467"
/db_xref="taxon:86956"

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BASE COUNT	/note="16S/23S_ribosome" RNA intergenic spacer region			
ORIGIN	257	121	187	159
a		c	g	t

Query Match	100.0%;	Score 724;	DB 1;	Length 724;
Best Local Similarity	100.0%;	Pred. No. 9.4e-105;		
Matches 724;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	gaagtcctgaacaaggtcagccgatactcggaaaggtgcgcgtcggatccactcccttcttaagat	60
Db	1	GAAGTCGTAAACAAGCTAGCCCGTATCGGAAGGTCCGGCTCGATCCACTCTTTCTTAAGAT	60
QY	61	lvgacaaaaactcgtctcagtagatccggaaatatgtatgttctgttcttgaaggtctcc	120
Db	61	TTTGACAAAAATCTGTCGAGTACATCCGGAAATATGTATTGTTTGTTGGTTTGAGGGTTTCC	120
QY	121	ctctaatatattagtaaggtacttgttaagagtggtttagtatagtttaaagcttgctcgg	180
Db	121	CTCTAATAAATATATAGTAGTACTTCTTAACAGAGTTTATGATATGTTTAAAAAGCTGGTCGG	180
QY	181	aaatattctgtgtgcacaaaaaagcaatggcagtagaagaagactcgtgcataaaaaaagaatgaac	240
Db	181	AAATATATTGTCGTGCAAAAAAATUCATTTGGCAGTACAGAAAGACTCGTAAAAAAGAATGAC	240
QY	241	taattgaggcgttagctcagatgtggaagagcacttgctcttcaagcagaggggtcagaagttc	300
Db	241	TAA TGCGGGCCCTAGCTCAGATGCGAGACACCTCGCTTGGAAAGCGGGGCTCAGAGTTC	300
QY	301	aactctcctcgtctccaccacaaagaagaaggccctatagctccagctggttagagcgacg	360
Db	301	AAC TCTCTCTGTTCTCACACAGACAGAAAGGCCCTATATAGCTCAGCTGGTTAAGCCGACG	360
QY	361	cccttgataagcgttgaggtcagtaacttcaagcttaacttaagccacccaatattgcacattga	420
Db	361	CCGTGATTAAGCGGTGAGAGTCACTAGTGTTCMAAGTCTTACTTAGCGCCACCACCATATTTGCACATTGA	420
QY	421	aaactacacagagaagaagcacaagaacaattacccaattgcacaacttgttaagaaatc	480
Db	421	AAACTACACACAGAGAAAGCAAGAACAATTTATCCAAATGGCCAAACTTTTAAGAGAAATC	480
QY	481	gagagagaataatggcggggaataagtgttgacaagaacaaatattagaaagaagaacaagct	540
Db	481	GAGGAGAAATGGCGGGGAATAGTTTGAACCCAGACCAAAATTTAGCAAAAAGAAACAACGCT	540
QY	541	aagaaacaaacataaaacttaagcgaaaaggtgatacttcgagagaagaacttaagagtt	600
Db	541	AAGAAACAACATATTAACCTTTAACCGCAAAAGCTGATATTCTTCGAGCAAACTTCAAGGTAT	600
QY	601	ataaacttaccagaagcgtttcagaatgcgagaagaagcgcaaaactctgagaagaagaagctat	660
Db	601	ATAAACTTACCAGAAGCGTTTCAGATTCGAGGAAGAGCGCAAAAGCTGAGAGAAAGCGTAT	660
QY	661	taatatcgtcgtgaatgaaacgaagcaaaacacattgcaaaagcagaatggaatggttatagggaag	720
Db	661	TAAATATACCGCTGATGAACGAAGCAAAACACTGACAAAGAGATGATGTTATGGAAGACT	720
QY	721	taca 724	
Db	721	TACA 724	

RESULT	2
AB022063	
LOCUS	AB022063
DEFINITION	Pectinatus frisingensis DNA, 16S/23S rRNA intergenic spacer region
ACCESSION	AB022063
VERSION	AB022063.1
KEYWORDS	GI:7288089

REFERENCE
1 (sites)
subdriacii; serenomonadaceae; pectinatus.

TITLE	JOURNAL	YEAR
16S-23S rDNA spacer of <i>Pectinatus</i> , <i>Selenomonas</i> and <i>Zymophilus</i> reveal new phylogenetic relationships between these genera	Int. J. Syst. Evol. Microbiol.	2000
	50 Pt 2, 883-886	
	20022199	

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 624)
Motoyama, Y. and Ogata, T.
Direct Submission
Submitted (07-JUN-1999) to the DDBJ/EMBL/GenBank databases. Tomcoo

FEATURES	Location/Qualifiers
source	1. .624

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/organism="Pectinatus frisingensis"
/strain="DSM6306"
/db_xref="taxon:865"
misc_feature
1..624

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BASE COUNT	ORIGIN	216 a	115 c	160 g	133 t	/note="16S/23S ribosomal RNA intergenic spacer region

Query Match	44.0%;	Score 318.8;	DB 1;	Length 624;
Best Local Similarity	87.2%;	Pred. No. 3.7e-41;		
Matches 441; Conservative	0;	Mismatches 57;	Indels	A: Gans 8

OY	221	ctcgtctaaaaaaagaaatgtgaactcaatctgagggcgtagctcaagaatggagagagacactgcctctgc	280
Db	119	ctcaaaaaaattgattgaaagaaactaatatggcgccctnactctgaactctggagagacactgcctcttgc	178
OY	281	aagcagcgagggttcacaggagttcacaactctcctctgcttcaccagaagaagaaa-ggcgctctatg	339
Db	179	aagcagggcgcttagagaggttcaaaatctcctctctccacgaagaaatggcgcttatg	238
OY	340	ctcagcttggttagagagcgagcgcttgataaagcgtgaagtcagtagttcaatctactaattg	399
Db	239	ctcagcttggttagagagcgagcgcttgataaagcgtgaagtcagtagttcaatctactaattg	298
OY	400	cccaaccaatctgtgacatcttgaaaaactacaagaag-aaagcaagaagaactt-atcacca	457
Db	299	cccaaccaatctgtgacatcttgaaaaactacaagaagaaagcaagaagaactt-aatcacca	358
OY	458	atgccaaactctgtaaga-gaaatcgaagagagaaatggcgggagatagttgaccaaagcac	516
Db	359	atgccaaactctgtagagagagaaatgttttcagagagatggcggggaatggttgaccaaagcac	418
OY	517	aaattagaaaaaagaaacaaacgcgtcaagaaacaaacatatataactctlaagcgaagaagtgtat	576
Db	419	-aatttagaamaacttaaaaaaacagcttaaacacaaacatattaaacttttaagc-taaaggtgat	475
OY	577	atctcgagagaaactctcaagat-atcaactctcagaagcgtctcaagttcgaggaagaag	635
Db	476	attctggagaggaactccagatcaatattaaattaaactttaccagaagcctttagatgcaaggaagac	535
OY	636	gcacaagctgagagaagaagcgtatataataacgctgataagcaagaacaaagcaactgcaca	695
Db	536	atgcaaacccgagatgcaagaaagccattatgattgattttagccgagatgagtgacttgaattgatagac	595

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SOURCE
1..467
/organism="Clostridium novyi"
/db_xref="ATCC25758"
complement(<1..30)
/product="16S ribosomal RNA"
complement(156..231)
/product="tRNA-Ala"
complement(239..315)
/product="tRNA-Ile"
complement(402..>467)
/product="23S ribosomal RNA"

BASE COUNT      139 a      84 c      112 g      132 t
ORIGIN

Query Match      16.2%; Score 117.6; DB 1; Length 467;
Best Local Similarity 82.6%; Pred. No. 1.5e-09;
Matches 147; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

QY 234 atgaactaagggcgtagctcagatgagagagcaccctccttgcagaagggtca 293
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 AATTTCATAGTACGGGCTATAGCTAGTGGAGACACCTGCTTGCACGCGGGGCTCA 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 294 ggaattcaactctcctcctccacccagaaagagagccctatagctcagctgtaga 353
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 AGACTTCGAATCTCTTATCTCCACACATA--CAATGCGCTATAGCTCAGCTGCTTACA 262
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 354 ggcgacgctcctataagcgtaggcagtagcttaagcttaagcttaagccccaatt 411
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 263 GCCACGCCCTGATTAAGCGGTGAGTGCATGTTGCGATGTCATTAGACCCACCATTTGTT 320
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
AB040726 417 bp DNA BCT 04-JAN-2001
LOCUS      Clostridium novyi genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA,
DEFINITION      partial and complete sequence.
ACCESSION      AB040726
VERSION      AB040726.1 GI:12039003
KEYWORDS      16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE      Clostridium novyi (strain:ATCC25758) DNA.
ORGANISM      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
              Clostridium.
REFERENCE      1 (sites)
AUTHORS      Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE      Rapid identification and differentiation of pathogenic clostridia
              in gas gangrene by polymerase chain reaction based on the 16S-23S r
              DNA spacer region
JOURNAL      Res. Vet. Sci. 69 (3), 289-294 (2000)
PUBMED      11124102
2 (bases 1 to 417)
DIRECT SUBMISSION
SUBMITTED (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
              Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
              185-8511, Japan (E-mail:sasakiy@vet.1.go.jp,
              Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..417
/organism="Clostridium novyi"
/db_xref="ATCC25758"
complement(<1..30)
/product="16S ribosomal RNA"
complement(106..181)
/product="tRNA-Ala"
complement(185..261)
/product="tRNA-Ile"
complement(352..>417)
/product="23S ribosomal RNA"

BASE COUNT      125 a      83 c      103 g      106 t
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ORIGIN

Query Match      16.2%; Score 117.4; DB 1; Length 417;
Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 167; Conservative 0; Mismatches 36; Indels 8; Gaps 2;

QY 243 atggggcgtagctcagatggaagagcactgccttcgaagggggtcagaagttcaa 302
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 ATGGGGGATAGCTCATTTGGAGAGACCTGCTTCACGACAGGGGCTCAAGATTGCA 163
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 303 ctctccctcgtccacccagaagaaggcctatagctcagctggttagagcgacgcc 362
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 164 ATCTCTTATCTCCACCA-----TAAGGCTTATAGCTCAGCTGTTAGAGCGCACGCC 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 363 tgataagcgtagctcagtagtcaagcttaagcttaagccccaatattgacattgaa 422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 TGATTAAGCTGAGCTGATGCTGATGCTCATTAGACCCACCA--ATTGTTCTTTGAAA 275
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 423 actacacagaagaagcaagaacaattalc 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 ATTGCACAGTGAATAAGAAACGAAAAAAC 306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
AB040737 514 bp DNA BCT 04-JAN-2001
LOCUS      Clostridium perfringens genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S
DEFINITION      rRNA, partial and complete sequence.
ACCESSION      AB040737
VERSION      AB040737.1 GI:12039014
KEYWORDS      16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE      Clostridium perfringens (strain:JCM1290) DNA.
ORGANISM      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
              Clostridium.
REFERENCE      1 (sites)
AUTHORS      Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE      Rapid identification and differentiation of pathogenic clostridia
              in gas gangrene by polymerase chain reaction based on the 16S-23S r
              DNA spacer region
JOURNAL      Res. Vet. Sci. 69 (3), 289-294 (2000)
PUBMED      11124102
2 (bases 1 to 514)
DIRECT SUBMISSION
SUBMITTED (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
              Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
              185-8511, Japan (E-mail:sasakiy@vet.1.go.jp,
              Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..514
/organism="Clostridium perfringens"
/db_xref="JCM1290"
complement(<1..30)
/product="16S ribosomal RNA"
complement(191..266)
/product="tRNA-Ala"
complement(272..348)
/product="tRNA-Ile"
complement(449..>514)
/product="23S ribosomal RNA"

BASE COUNT      170 a      95 c      115 g      134 t
ORIGIN

Query Match      16.2%; Score 117.4; DB 1; Length 514;
Best Local Similarity 77.9%; Pred. No. 1.6e-09;
Matches 169; Conservative 0; Mismatches 41; Indels 7; Gaps 2;

QY 243 atggggcgtagctcagatggaagagcactgccttcgaagggggtcagaagttcaa 302
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 189 ATGGGGGATATAGCTTAGTTGGAGAGCACTGGCCCTTGACCCAGAGGGGTCAGCAGTTGCA 248

OY 303 CTCTCTCTCTCTCCACCAGAGAGAAAGCGCTAGCTCAGCTCGTGTAGAGCGCAGCC 362

Db 249 ATCTCTCTTACCTGCCACCATATG----TGGGTCTATAGCTCAGGTGGTTAAAGCCGACGCG 304

OY 363 TATAAGCTGTAGAGTCAGTAGTCAAGTCTCCTTAGGCCACCATATGCATATGAA 422

Db 305 TCGATTAAGCTGACGCTCGATCGCTTGACGTCATTTAAGACCCAGCC---ATTGTTCTTTGAAA 361

OY 423 actacacagagaagaagcaaaagaacatattaccat 459

Db 362 ATTGGACATTAATTATATATATAAACAACAAGCCCAAT 398

RESULT	10
LOCUS	AB040729
DEFINITION	AB040729 413 bp DNA BCF 04-JAN-2001
ACCESSION	AB040729.1
VERSION	1
KEYWORDS	16S ribosomal RNA; 23S rRNA; 23S rRNA.
SOURCE	<i>Clasidium haemolyticum</i> (strain:ATCC9650) DNA.
ORGANISM	<i>Clasidium haemolyticum</i>

REFERENCE
AUTHORS
TITLE

1 (sites)
Sasaki, Y., Yamamoto, K., Kojima, A., Norimatsu, M. and Tamura, Y.
Rapid identification and differentiation of *Neisseria meningitidis* strains by polymerase chain reaction

in gas gangrene by polymerase chain reaction based on the 16S-23S rDNA spacer region
Res. Vet. Sci. 69 (3), 289-294 (2000)

2 (cases 1 to 415)
Sasaki, Y. and Tamura, Y
Direct Submission
Submitted (26-MAR-2000)
JOURNAL

185-8511, Japan (E-mail: sasaki@val.go.jp,
Tel: +81-42-321-1841 (ex.230), Fax: +81-42-321-1769)
Location/Qualifiers

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/organism="Clostridium haemolyticum
/strain="ARCC9650"
/db_xref="taxon:84025"
complement(<1..30)
/product="16S ribosomal RNA"
complement(106..181)
/product="tRNA-Ala"
complement(185..261)
/product="tRNA-Ile"
complement(348..>413)
/product="23S ribosomal RNA"
BASE COUNT      121 a      82 c      103 g      107 t
ORIGIN

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Query Match	15.8%;	Score 114.2;	DB 1;	Length 413;
Best Local Similarity	79.5%;	Pred. No. 5.3e-09;		
Matches 163;	Conservative 0;	Mismatches 33;	Indels 9;	Gaps 2

243 a tgggggcgcagtcacaaatggagagacacctccttgcgaagaagggtctcaggttcaa 302

104 atggggcgtatagctcattggcagacacctcccttcacagcaggggtcaaggattcga 163

303 cttcccccgcgtctcaccagaagaaggcctatagctcagttggtttagagcagcc 362

164 atgcctttatctccacca-----tagagctctatagctcactctgttagcgcacgcc 217

363 tgcataagcgcgaagtcagttgattcaagctactctaggccccaacataltgacattgaa 422

218 tgcattacgcgagacctgcattgctcagctcatttagaccaccac-----attgctcttttgaaa 274

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QY      423  actacacagaagaagcaagaaca  447
          | | |||| | | || | |
Db      275  ATTGCACAGTGATAAGAAACGAAA  299

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RESULT	11
AB040724	
LOCUS	505 bp DNA
DEFINITION	Clostridium novyi genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA partial and complete sequence.
ACCESSION	AB040724
VERSION	AB040724.1
KEYWORDS	GI:12039001
SOURCE	16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
ORGANISM	Clostridium novyi (strain:JCM1406) DNA.

REFERENCE	AUTHORS	TITLE	JOURNAL	PIRMEED
1	Sasaki, Y., Yamamoto, K., Kojima, A., Norimatsu, M. and Tamura, Y.	Rapid identification and differentiation of pathogenic clostridia in gas gangrene by polymerase chain reaction based on the 16S-23S rDNA spacer region	Res. Vet. Sci. 65 (3), 289-294 (2000)	11124105

REFERENCE	2 (bases 1 to 505)
AUTHORS	Sasaki, Y. and Tamura, Y.
TITLE	Direct Submission
JOURNAL	Submitted (26-MAR-2000)

185-8511, Japan (E-mail: sasakiy@naval.go.jp,
Tel: +81-42-321-1841 (ex. 230), Fax: +81-42-321-1769)
Location/Qualifiers

BASE COUNT	157	92	118	138
ORIGIN	a	c	g	t
/organism="Clostridium novy				
/strain="JCM1406"				
/db_xref="taxon:1542"				
complement<1..30)				
/product="16S ribosomal RNA"				
complement(157..232)				
/product="tRNA ^{Ala} "				
complement(236..312)				
/product="tRNA ^{Ile} "				
complement(440..>505)				
/product="23S ribosomal RNA"				

Query Match	15.78;	Score	113.8;	DB 1;	Length	505;
Best Local Similarity	74.98;	Pred. No.	5.8e-09;			
Matches	158;	Conservative	0;	Mismatches	47;	
				Totals	6;	Cover
					1	

[illegible]

RESULT 12
CJ16SRNA
LOCUS CJ16SRNA 5996 bp DNA BCT 04-MAR-1996

DEFINITION C.jejuni TGH9011(ATCC43431) gene for ribosomal RNA operon.
 VERSION 229326
 KEYWORDS 16S ribosomal RNA; 23S ribosomal RNA; 5S ribosomal RNA; transfer RNA-Ala; transfer RNA-Ile.
 SOURCE Campylobacter jejuni.
 ORGANISM Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
 REFERENCE 1 (bases 1 to 5996)
 AUTHORS Kim, N.W., Gutell, R.R. and Chan, V.L.
 TITLE Complete sequences and organization of the rRNA operon from Campylobacter jejuni TGH9011 (ATCC43431)
 JOURNAL Gene 164 (1), 101-106 (1995)
 MEDLINE 96060846
 REFERENCE 2 (bases 1 to 5996)
 AUTHORS Chan, V.V.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-1994) Chan V. V., University of Toronto, Microbiology, 150 College Street, Toronto, Ontario, Canada, M5S 1A8
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 ORIGIN

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 Best Local Similarity 74.4%; Pred. No. 5.9e-09;
 Matches 154; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 217 aagactgtaaaaaaagaatgaactaatatggggcgtagctcaatgtagagcactgccc 276
 DB 1853 AAGATTGATCATTAAGCTAATGTTATGGGGAATTAGCTACAGCTGGAGAGCGCTGCT 1912
 QY 277 ttgcaagcagggggtcaggaggttcaactctccgcgtccaccagaagaaggagccta 336
 DB 1913 TTGCACCCAGAGAGTCAGCGTTCTGATCCCGTATTCTCCACCA-TTTATTAAAGGCCCTA 1971
 QY 337 tagctcagctgtgttaagcgcagcctgataagcgtgaagtcagttcaagttcactt 396
 DB 1972 TAGCTCAGCTGTTAGACGTCACCCCTGATTAAGGCTGACAGTTCAGAGTTCAAGTCTGTT 2031
 QY 397 agggccaccacaatattgcacattgaaaa 423
 DB 2032 AGGCCACCACTTAATAAAAGATTTCGAATA 2058
 RESULT 13
 LOCUS Cj11168X2 308601 bp DNA 08-JUL-2000
 DEFINITION Campylobacter jejuni NCTC11168 complete genome; segment 2/6.
 ACCESSION AL139075 AL111168
 VERSION AL139075.2 GI:6967817
 KEYWORDS
 SOURCE
 ORGANISM
 Campylobacter jejuni.
 Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
 1 (bases 1 to 308601)
 Parkhill, J., Wren, B.W., Mungall, K., Ketley, J.M., Churcher, C., Basham, D., Chillingworth, T., Davies, R.M., Feltham, T., Holtroft, S., Jagels, K., Karlyshev, A., Moule, S., Pallen, M.J., Penn, C.W., Quail, M., Rajandream, M.A., Rutherford, K.M., VanNiel, A., Whitehead, S. and Barrett, B.C.
 The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences
 Nature 403 (6770), 665-668 (2000)
 2 (bases 1 to 308601)
 Parkhill, J.
 Direct Submission
 Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire CB10 1SA E-mail: parkhill@sanger.ac.uk
 COMMENT
 Details of C. jejuni sequencing at the Sanger Centre are available on the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/C._jejuni/).
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 CDS

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    2546..3103
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    /codon_start=1
    /transl_table=11
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    /note="Cj0348, trpB, probable tryptophan synthase beta chain, len: 392 aa; highly similar to many e.g. TRPB_THEMA tryptophan synthase beta chain (EC 4.2.1.20) (389 aa), fasta scores: opt: 1476 z-score: 2082.2 E(): 0, 59.9% identity in 384 aa overlap, 56.4% identity to HP1278. Contains PS00168 Tryptophan synthase beta chain pyridoxal-phosphate attachment site, PS00017 ATP/GTP-binding site motif A (P-loop), and pfam match to entry PF00247 trp-syntB, tryptophan synthases, beta chain, score 806.40, E-value 1e-238"
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    /transl_table=11
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    /db_xref="GI:6967823"
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Query Match      15.4%; Score 111.8; Db 1; Length 308601;
Best Local Similarity 74.4%; Pred. No. 1.9e-09;
Matches 154; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

OY 217 aagactgtaaaagaagaactaataatgggggagctagctcacatggaagaacactgcc 276
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Db 81620 AAGTTCATGATTAAGCTAATGTTTATGGGAGATTAGCTACGTGGAGAGCGCCGTCT 81679

OY 277 ttgcaagcagggggtcagggagttcaactctcctcgtctccacacagaagaagaaggccca 336
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Db 81680 TTGGACCCACGAGAGCTGACCGCTTCGATCCCGCTATTCTCCACCA-TTTATTAGGGCCCTA 81738

OY 337 tagctcagctggttagagcgacgacctgataacgctgagagtgcttagtcaacttactt 396
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81739 TAGCTCAGCTGCTTAGAGTCACTACCCCTGATTAAGGAGGTGAGGTCAAGTCTTGT 81798

OY 397 aggcacacaaatattgcacattgaana 423
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Db 81799 AGGCCACCATATAAAGATTGATTA 81825

RESULT 14
LOCUS Cj11168X1 314150 bp DNA
DEFINITION Campylobacter jejuni NCTC11168 complete genome; segment 1/6.
ACCESSION AL139074 AL111168
VERSION AL139074.2 GI:6967505
KEYWORDS
SOURCE
ORGANISM Campylobacter jejuni.
          Campylobacter jejuni.
          Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
          Campylobacter.
REFERENCE 1 (bases 1 to 314150)
          Parshall,J., Wren,B.W., Mungall,K., Ketley,J.M., Churcher,C.,
          Basham,D., Chillingworth,T., Davies,R.M., Feltham,T., Holtroyd,S.,
          Jagels,K., Kariyeh,A., Moule,S., Pallen,M.J., Penn,C.W.,
          Quail,M., Rajandream,M.A., Rutherford,K.M., VanVleet,A.,
          Whitehead,S. and Barrett,B.G.
          The genome sequence of the food-borne pathogen Campylobacter jejuni
          reveals hypervariable sequences
          Nature 403 (6770), 665-668 (2000)
2 (bases 1 to 314150)
          Parkhill,J.
          Direct Submission
          Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter
          Sequencing Team, Sanger Centre, Wellcome Trust Genome Campus,
          Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT
          Notes:
          Details of C. jejuni sequencing at the Sanger Centre are available
          on the World Wide Web.
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              /note="Cj0001, dnaA, probable chromosomal replication
              initiator protein, len: 440 aa; similar to many e.g.
              DNA_ECOLI (467 aa), fasta scores: opt. 839 z-score: 949.6
              E(): 0, 32.3% identity in 470 aa overlap, 39.9% identity
              to Hpi1529. Contains P80017 ATP/GTP-binding site motif A
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              Bacterial dnaA protein, score 419.90, E-value 4e-141"
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FEFFIENIKNNDGQIIMTSNPMKLGICIERLKSRAH8ITADITPOLDKTAIR
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301. .1239
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427. .450
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1483. .2535
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1483. .2550
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/note="Cj0002, dnaN, probable DNA polymerase III, beta
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polymerase III, beta chain (EC 2.7.7.7) (366 aa), fasta
scores: opt. 349 z-score: 372.3 E(): 1.7e-13, 19.6%
identity in 367 aa overlap, 34.2% identity to Hb0500.
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2579. .4888
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/note="Cj0003, gyrB, probable DNA gyrase subunit B, len:
769 aa; similar to many e.g. GYRB_BACSU DNA gyrase subunit
B (EC 5.99.1.3) (638 aa), fasta scores: opt. 2130 z-score:
3165.8 E(): 0, 47.7% identity in 773 aa overlap, 61.2%
identity to Hp0501. Contains P80017 DNA topoisomerase II
signature and Pflam matches to entry PF00204 DNA_topoII,
DNA topoisomerase II (N-terminal region), score 915.20,
E-value 1.9e-271, and to entry PF00986 DNA_gyraseB_C, DNA
gyrase B subunit, carboxyl terminus, score 154.00, E-value
2.6e-42"
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GISQDFVFNKKKEALTKAIFESVDEEDVNVNVALINDYTSENLSFVNNTITPDGT
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3830. .3856

/gene="gyrB"

/note="P50017 DNA topoisomerase II signature"

4649. .4852

/gene="gyrB"

/note="Pfam match to entry PF00986 DNA gyraseB, C, DNA gyrase B subunit, carboxyl terminus, score 154.00, E-value 2.6e-42"

complement(4916. .5257)

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complement(4916. .5257)

/note="Cj0004c", possible periplasmic protein, len: 113 aa, No Hp match. Contains possible N-terminal signal sequence"

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complement(5260. .6498)

/gene="Cj0005c"

complement(5260. .6498)

/note="Cj0005c", possible molybdenum containing oxidoreductase, len: 412 aa; similar to many eukaryotic oxidoreductases e.g. SUOX, HUMAN sulfite oxidase precursor (488 aa), fasta scores: opt: 543 z-score: 338.2 E(): 1.4e-11, 29.8% identity in 372 aa overlap and NIA-PTNH nitrate reductase from Petunia hybrida (909 aa), fasta scores: opt: 281 z-score: 312.5 E(): 3.8e-10, 28.9% identity in 395 aa overlap. No Hp match. Contains Pfam match to entry PF00174 oxidored.molyb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

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/transl_table=11

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/db_xref="GI:6967510"

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complement(5950. .6138)

/gene="Cj0005c"

/note="Pfam match to entry PF00174 oxidored.molyb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

6703. .8010

/gene="Cj0006"

6703. .8010

/gene="Cj0006"

/note="Cj0006", probable integral membrane protein, len: 435 aa; similar to e.g. Y325-HAfin hypothetical protein

misc_feature

/note="Pfam match to entry PF00204 DNA topoisom. II (N-terminal region), score 915.20, E-value 1.9e-271"

3830. .3856

/gene="gyrB"

/note="P50017 DNA topoisomerase II signature"

4649. .4852

/gene="gyrB"

/note="Pfam match to entry PF00986 DNA gyraseB, C, DNA gyrase B subunit, carboxyl terminus, score 154.00, E-value 2.6e-42"

complement(4916. .5257)

/gene="Cj0004c"

complement(4916. .5257)

/note="Cj0004c", possible periplasmic protein, len: 113 aa, No Hp match. Contains possible N-terminal signal sequence"

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/transl_table=11

/product="putative periplasmic protein"

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/db_xref="GI:6967509"

/translation="MKKIIILALFLASMAQNLINPDGLIIDPSPIVANCILAC HSNLLNNHSAKRMALAIIRMQDSELMIEPEDEKILNLKTYGKEDTRRI PLAILLONTH"

complement(5260. .6498)

/gene="Cj0005c"

complement(5260. .6498)

/note="Cj0005c", possible molybdenum containing oxidoreductase, len: 412 aa; similar to many eukaryotic oxidoreductases e.g. SUOX, HUMAN sulfite oxidase precursor (488 aa), fasta scores: opt: 543 z-score: 338.2 E(): 1.4e-11, 29.8% identity in 372 aa overlap and NIA-PTNH nitrate reductase from Petunia hybrida (909 aa), fasta scores: opt: 281 z-score: 312.5 E(): 3.8e-10, 28.9% identity in 395 aa overlap. No Hp match. Contains Pfam match to entry PF00174 oxidored.molyb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

/codon_start=1

/transl_table=11

/product="putative molybdenum containing oxidoreductase"

/protein_id="CAB72498.1"

/db_xref="GI:6967510"

/translation="MKQNDQKRNRRDLFLNKINIGLFGISVLNFSFENPLGSKALAKE LPHRIEKKKQILYHGKRPPLAETELIYALDSDDTPKPFNFVNNNGIPSTELIKRLR KGWLEIDSGYILNKKSYTIEDLKKEKRYTVALTECGGNSRSYIPSTGTOMGTG AVACGRMGVGLKIDLKDCGKINDAVYIGCYGIDTRLKNEETSPISGVPSKALQDE TLIMAAEGKQDPLVNYGRLPRLVCGGTPASTSKWLYIKTSVNNKLIHDEKMSKKVP VNPKRQDFNFKGEMKLTIESMPLRSVITNINKNSSEIKRKKRFEVAGKMADELEVSV YVSDYGTQWTKRAVEKPLNRLAMQKWSAQISLPTKGYEITIMARAIDSGQSNQWVLA QMNQCGYINNAACHVNVYGV"

complement(5950. .6138)

/gene="Cj0005c"

/note="Pfam match to entry PF00174 oxidored.molyb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

6703. .8010

/gene="Cj0006"

6703. .8010

/gene="Cj0006"

/note="Cj0006", probable integral membrane protein, len: 435 aa; similar to e.g. Y325-HAfin hypothetical protein

Query Match	15.4%	Score 11.8	DB 1	Length 314150
Best Local Similarity	74.4%	Pred. No. 1.9e-09		
Matches 154	Conservative	0	Mismatches 52	Indels 1 Gaps 1
				/product="putative integral membrane protein"
Qy 217	aagacggtgaataaaagaatgaactaatatggggcgtagctcagatgtaggaagacactgcc	276		
Db 40838	AAATTTGATGATATAACCTATTGTTATTTGGCGAATTAGCTCAGCTCGGACGCCGCTCT	40897		
Qy 277	tgcgaagcagggggtcagaagatcgaactctccctgcgtccaccagagaagaaggcccta	336		
Db 40898	TTTCACAGCAGAGAGCTAGCGGTTTCGATCCCGCTATTCTCCACCA-TTTATTAAAGGCGCTA	40936		
Qy 337	tagctagcttggttaagcagcagcgcctgataagcgtgaagtcagtagtcaagtctact	396		
Db 40957	TAGCTAGCTGGTTAAGTAGTCACCCCTGATAAGGAGTGAAGTCAAGTTCAAGTCTGTT	41016		
Qy 397	aggccaccacatatgcatcatgaa 423			
Db 41017	AGGCCACCATTAATAAAGATTGAAATA 41043			
RESULT 15				
LOCUS	CJ11168X3	317511 bp	DNA	BCF 08-JUL-2000
DEFINITION	Campylobacter jejuni NCTC11168 complete genome; segment 3/6.			
ACCESSION	AL139076	AL111168		
VERSION	AL139076.2	GI:5968128		
KEYWORDS				
SOURCE				
ORGANISM	Campylobacter jejuni. Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter jejuni. Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.			
REFERENCE	1 (bases 1 to 317511) Parkhill,J., Wren,B.W., Mungall,K., Ketley,J.M., Churcher,C., Basham,D., Chillingworth,T., Davies,R.M., Feltwell,T., Holtroyd,S., Jagels,K., Karlyshev,A., Moule,S., Pallen,M.J., Penn,C.W., Quail,M., Rajandream,M.A., Rutherford,K.M., Vanyilet,A., Whitehead,S. and Barrall,B.G. The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences Nature 403 (6770), 665-668 (2000)			
TITLE	2 (bases 1 to 317511) Parkhill,J. Direct Submission Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg CB10 1SA E-mail: parkhill@sanger.ac.uk			
JOURNAL				
MEDLINE				
REFERENCE				
AUTHORS				
TITLE				
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COMMENT				
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gene				
CDS				

